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Sequence Listing was accepted.

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Reviewer: Durreshwar Anjum

Timestamp: [year=2009; month=11; day=10; hr=11; min=57; sec=2; ms=344;]

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Application No: 10597914 Version No: 2.0

Input Set:

Output Set:

Started: 2009-11-09 14:23:43.802
Finished: 2009-11-09 14:23:51.526
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 724 ms
Total Warnings: 111
Total Errors: 0
No. of SeqIDs Defined: 111
Actual SeqID Count: 111

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
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W 402	Undefined organism found in <213> in SEQ ID (9)
W 402	Undefined organism found in <213> in SEQ ID (10)
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W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (20)

Input Set:

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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (51)
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W 213	Artificial or Unknown found in <213> in SEQ ID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
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W 213	Artificial or Unknown found in <213> in SEQ ID (57)
W 213	Artificial or Unknown found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
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	This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Representative: Greenlee, Winner and Sullivan, P.C.
HODGES, Robert S
TRIPET, Brian

<120> COMPOSITIONS AND METHODS FOR MODIFICATION AND PREVENTION OF SARS
CORONAVIRUS INFECTIVITY

<130> 6-04

<140> 10597914

<141> 2009-11-09

<150> US 60/544,410

<151> 2004-02-12

<150> PCT US05/004408

<151> 2005-02-14

<160> 111

<170> PatentIn version 3.5

<210> 1

<211> 3768

<212> DNA

<213> SARS coronavirus Urbani

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Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30

cat act tca tct atg agg ggg gtt tac tat cct gat gaa att ttt aga 144
His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45

tca gac act ctt tat tta act cag gat tta ttt ctt cca ttt tat tct 192
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60

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Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80

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Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn			
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Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln			
100	105	110	
tcg gtg att att aac aat tct act aat gtt gtt ata cga gca tgt			384
Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys			
115	120	125	
aac ttt gaa ttg tgt gac aac cct ttc ttt gct gtt tct aaa ccc atg			432
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met			
130	135	140	
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Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr			
145	150	155	160
ttc gag tac ata tct gat gcc ttt tcg ctt gat gtt tca gaa aag tca			528
Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser			
165	170	175	
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Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly			
180	185	190	
ttt ctc tat gtt tat aag ggc tat caa cct ata gat gta gtt cgt gat			624
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp			
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cta cct tct ggt ttt aac act ttg aaa cct att ttt aag ttg cct ctt			672
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Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Tyr Phe Val Gly Tyr			
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Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile			
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Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys			
275	280	285	
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Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn			
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325	330	335		
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Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr				
340	345	350		
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355	360	365		
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Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala				
370	375	380		
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385	390	395	400	
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Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe				
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Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu				
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Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly				
450	455	460		
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Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp				
465	470	475	480	
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Tyr Gly Phe Tyr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val				
485	490	495		
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Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly				
500	505	510		
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Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn				
515	520	525		
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tcc gtt cga gat cct aaa aca tct gaa ata tta gac att tca cct tgc Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys	565	570	575		1728
tct ttt ggg ggt gta agt gta att aca cct gga aca aat gct tca tct Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser	580	585	590		1776
gaa gtt gct gtt cta tat caa gat gtt aac tgc act gat gtt tct aca Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr	595	600	605		1824
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gga aac aat gta ttc cag act caa gca ggc tgt ctt ata gga gct gag Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu	625	630	635	640	1920
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act aca gaa gta atg cct gtt tct atg gct aaa acc tcc gta gat tgt Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys	705	710	715	720	2160
aat atg tac atc tgc gga gat tct act gaa tgt gct aat ttg ctt ctc Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu	725	730	735		2208
caa tat ggt agc ttt tgc aca caa cta aat cgt gca ctc tca ggt att Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile	740	745	750		2256
gct gct gaa cag gat cgc aac aca cgt gaa gtg ttc gct caa gtc aaa Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys	755	760	765		2304

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Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala

995

1000

1005

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ccg cat ggt gtt gtc ttc cta cat gtc acg tat gtg cca tcc cag 3159
Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
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Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
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gca tac ttc cct cgt gaa ggt gtt ttt gtg ttt aat ggc act tct 3249
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Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
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